(f) identifying with respect to the reference sequence one or more of a mutation, a mutation distribution, a mutation frequency, sequence heterogeneity, or DNA damage.

40. The method of claim **39**, wherein the sample is derived from a human.

41. The method of claim **39**, wherein the sample comprises a tissue sample.

42. The method of claim **39**, wherein the sample comprises a blood sample.

43. The method of claim **39**, wherein the method comprises detecting mutations or DNA damage that arose in vivo.

44. The method of claim **39**, wherein the DNA damaging agent comprises a chemotherapy agent.

45. The method of claim **39**, further comprising comparing the first-strand sequencing reads with the second-strand sequencing reads, and generating error-corrected sequences of the double-stranded DNA molecules by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand.

46. The method of claim **45**, further comprising calculating a mutation frequency among the plurality of double-stranded DNA molecules.

47. The method of claim **46**, wherein the mutation is a transition mutation.

48. The method of claim **45**, wherein an error-corrected sequence maps to the reference sequence, and wherein a sequence difference between the error-corrected sequence and the reference sequence is identified as a true mutation.

49. The method of claim **48**, wherein the true mutation is a substitution or insertion mutation type.

50. The method of claim **48**, wherein the true mutation is a transition mutation.

51. The method of claim **45**, wherein the error-corrected sequences map to the reference sequence, and the method further comprises identifying a distribution of mutations in the double-stranded DNA molecules.

52. The method of claim **49**, wherein the error-corrected sequences map to the reference sequence, and the method further comprises identifying a distribution of mutation types in the double-stranded DNA molecules.

53. The method of claim **45**, wherein the erroneous nucleotides in one strand that lack a matched base change in the complementary strand are the result of systematic or biological errors in one strand.

54. The method of claim **45**, wherein the method comprises determining a genomic distribution of mutations with respect to the reference sequence.

55. The method of claim **54**, further comprising identifying mutations common to most cells of a tumor.

56. The method of claim **54**, further comprising determining whether a genomic distribution of mutations is a random distribution.

57. The method of claim **39**, further comprising comparing the first-strand sequencing reads with the second-strand sequencing reads to generate error-corrected sequences, and reconstructing original double-stranded DNA sequences from the error-corrected sequences.

58. The method of claim **39**, wherein the double-stranded DNA molecules comprise a deaminated cytosine.

59. The method of claim **58**, wherein the method further comprises enzymatically treating the double-stranded DNA molecules to repair damaged ends thereof prior to the ligating.

60. The method of claim **39**, further comprising purifying a plurality of cypher-target nucleic acid complexes prior to sequencing, wherein the purified cypher-target nucleic acid complexes comprise nucleic acid molecules from specific genomic regions.

61. The method of claim **39**, wherein prior to the mapping, the method further comprises grouping sequencing reads based on (i) the identifier tag sequences and (ii) sequence information from the double-stranded DNA molecules, wherein a group comprises sequencing reads from the cypher-target amplification products of one of the cypher-target nucleic acid complexes.

62. The method of claim **39**, wherein the cypher-target nucleic acid complexes comprise asymmetrical complexes having identifier tags of different lengths at each end.

63. The method of claim **39**, wherein the cypher polynucleotides comprise a capture sequence and the sequencing comprises capturing the amplified cypher-target nucleic acid complexes on a solid surface comprising primers complementary to the capture sequence.

64. The method of claim **39**, wherein the identifier tag sequences comprise random or partially random sequences.

65. The method of claim **64**, wherein the random or partially random sequences comprise a length from about 5 nucleotides to about 50 nucleotides.

66. The method of claim **64**, wherein the identifier tags are double-stranded sequences.

67. The method of claim **39**, wherein the mutation, mutation distribution, mutation frequency, sequence heterogeneity, or DNA damage comprises a cancer biomarker.

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